

IN THE CLAIMS

Please amend the claims as follows:

Claims 1-10 (Cancelled).

11. (New) A method of amplifying RNA of a small round structured virus, comprising reverse transcribing said RNA to DNA with at least one primer comprising at least 10 contiguous bases of a sequence selected from the group consisting of SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, and SEQ ID NO:31.

12. (New) The method of Claim 11, further comprising amplifying said DNA with at least one first primer and at least one second primer, wherein said first primer comprises at least 10 contiguous bases of a sequence selected from the group consisting of SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, and SEQ ID NO:24; and said second primer comprises at least 10 contiguous bases of a sequence selected from the group consisting of SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, and SEQ ID NO:31.

13. (New) The method of Claim 12, wherein at least one of said first primer and second primer further comprises an RNA polymerase promoter, and said method further comprises transcribing the DNA after said amplification.

14. (New) The method of Claim 11, wherein said primer comprises at least 10 contiguous bases of SEQ ID NO:20 or SEQ ID NO:28.

15. (New) The method of Claim 11, wherein said primer comprises at least 10 contiguous bases of SEQ ID NO:20.

16. (New) The method of Claim 11, wherein said primer comprises at least 10 contiguous bases of SEQ ID NO:28.

17. (New) The method of Claim 12, wherein said first primer comprises at least 10 contiguous bases of SEQ ID NO:20.

18. (New) The method of Claim 12, wherein said second primer comprises at least 10 contiguous bases of SEQ ID NO:28.

19. (New) A method of detecting the presence of a small round structured virus in a sample, comprising reverse transcribing RNA of the small round structured virus to DNA with at least one primer comprising at least 10 contiguous bases of a sequence selected from the group consisting of SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, and SEQ ID NO:31; and detecting the presence of the DNA, which is indicative of the presence of the small round structured virus in the sample.

20. (New) The method of Claim 19, further comprising, before detecting the presence of the DNA, amplifying said DNA with at least one first primer and at least one second primer, wherein said first primer comprises at least 10 contiguous bases of a sequence selected from the group consisting of SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, and SEQ ID NO:24; and said second primer comprises at least 10 contiguous bases of a sequence selected from the group consisting of SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, and SEQ ID NO:31.

21. (New) The method of Claim 19, wherein detecting the presence of DNA comprises hybridizing the DNA with at least one probe comprising at least 10 contiguous bases of a sequence selected from the group consisting of SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, and SEQ ID NO:35.

22. (New) The method of Claim 21, wherein said probe is fluorescently labeled.

23. (New) The method of Claim 21, wherein said probe is labeled with a fluorescent label which exhibits a different fluorescent property when the probe is hybridized with the DNA compared to when the probe is not hybridized to the DNA.

24. (New) The method of Claim 21, wherein said probe comprises at least 10 contiguous bases of SEQ ID NO:35.

25. (New) The method of Claim 19, wherein said primer comprises at least 10 contiguous bases of SEQ ID NO:20 or SEQ ID NO:28.

26. (New) The method of Claim 19, wherein said primer comprises at least 10 contiguous bases of SEQ ID NO:20.

27. (New) The method of Claim 19, wherein said primer comprises at least 10 contiguous bases of SEQ ID NO:28.

28. (New) The method of Claim 20, wherein said first primer comprises at least 10 contiguous bases of SEQ ID NO:20.

29. (New) The method of Claim 20, wherein said second primer comprises at least 10 contiguous bases of SEQ ID NO:28.

30. (New) A method of detecting the presence of a small round structured virus in a sample, comprising

reverse transcribing RNA small round structured virus of said to DNA with at least one primer comprising at least 10 contiguous bases of a sequence selected from the group consisting of SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, and SEQ ID NO:31;

amplifying said DNA with at least one first primer and at least one second primer, wherein said first primer comprises at least 10 contiguous bases of a sequence selected from the group consisting of SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, and SEQ ID NO:24; and said second primer comprises at least 10 contiguous bases of a sequence selected from the group consisting of SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, and SEQ ID NO:31, wherein at least one of said first primer and said second primer further comprises an RNA promoter;

transcribing the DNA to RNA after said amplification; and
detecting the presence of the RNA, which is indicative of the presence of the small round structured virus in the sample.

31. (New) The method of Claim 30, wherein detecting the presence of RNA comprises hybridizing the RNA with at least one probe comprising at least 10 contiguous bases of a sequence selected from the group consisting of SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, and SEQ ID NO:35.

32. (New) The method of Claim 31, wherein said probe is fluorescently labeled.

33. (New) The method of Claim 31, wherein said probe is labeled with a fluorescent label which exhibits a different fluorescent property when the probe is hybridized with the RNA compared to when the probe is not hybridized to the RNA.

34. (New) The method of Claim 31, wherein said probe comprises at least 10 contiguous bases of SEQ ID NO:35.

35. (New) The method of Claim 30, wherein said primer used for reverse transcribing comprises at least 10 contiguous bases of SEQ ID NO:20 or SEQ ID NO:28.

36. (New) The method of Claim 30, wherein said primer used for reverse transcribing comprises at least 10 contiguous bases of SEQ ID NO:20.

37. (New) The method of Claim 30, wherein said primer used for reverse transcribing comprises at least 10 contiguous bases of SEQ ID NO:28.

38. (New) The method of Claim 30, wherein said first primer comprises at least 10 contiguous bases of SEQ ID NO:20.

39. (New) The method of Claim 30, wherein said second primer comprises at least 10 contiguous bases of SEQ ID NO:28.